

SEQUENCE LISTING

<110> Jaworski, Jan G.
Blacklock, Brenda J.

<120> FATTY ACID ELONGASE 3-KETOACYL COA
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<151> 2000-06-08

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Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	
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gcc	tct	cgg	ctt	acc	ata	aac	gat	ctc	cac	aac	ttc	ctt	tcc	tat	ctc	144
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	
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Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	
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Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	
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Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
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 35 40 45
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 50 55 60
 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
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 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
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 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
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 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
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 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
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 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu
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 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met

60
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His Leu Tyr Tyr Ser Tyr Leu Gln His Asn Leu Ile Thr Ile Ala Pro	
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Leu Leu Ala Phe Thr Val Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg	
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Pro Lys Pro Val Tyr Leu Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr	
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aac	aag	cct	aga	gat	cgt	aga	cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	975	
Asn	Lys	Pro	Arg	Asp	Arg	Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr		
			285					290						295			
gtt	cga	acg	cat	acc	gga	gct	gac	gac	aag	tct	ttt	cgt	tgc	gtg	caa	1023	
Val	Arg	Thr	His	Thr	Gly	Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln		
			300				305						310				
caa	gga	gac	gat	gag	aac	ggc	caa	acc	gga	gtg	agt	ttg	tcc	aag	gac	1071	
Gln	Gly	Asp	Asp	Glu	Asn	Gly	Gln	Thr	Gly	Val	Ser	Leu	Ser	Lys	Asp		
			315			320						325					
ata	acc	gat	gtt	gct	ggc	cga	acg	gtt	aag	aaa	aac	ata	gca	acg	ctg	1119	
Ile	Thr	Asp	Val	Ala	Gly	Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu		
					335					340					345		
ggc	ccg	ttg	att	ctt	ccg	tta	agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	1167	
Gly	Pro	Leu	Ile	Leu	Pro	Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr		
				350					355					360			
ttc	atg	ggc	aag	aaa	ctt	ttc	aaa	gac	gaa	atc	aaa	cat	tat	tac	gtc	1215	
Phe	Met	Gly	Lys	Lys	Leu	Phe	Lys	Asp	Glu	Ile	Lys	His	Tyr	Tyr	Val		
			365					370					375				
ccg	gac	ttc	aag	ctt	gct	atc	gac	cat	ttt	tgt	ata	cat	gcc	gga	ggc	1263	
Pro	Asp	Phe	Lys	Leu	Ala	Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly		
			380				385					390					
aaa	gcc	gtg	att	gat	gtg	cta	gag	aag	aac	cta	ggc	cta	gca	ccg	atc	1311	
Lys	Ala	Val	Ile	Asp	Val	Leu	Glu	Lys	Asn	Leu	Gly	Leu	Ala	Pro	Ile		
			395			400					405						
gat	gta	gag	gca	tca	aga	tca	acg	tta	cat	aga	ttt	gga	aac	act	tca	1359	
Asp	Val	Glu	Ala	Ser	Arg	Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser		
					415					420					425		
tct	agc	tca	ata	tgg	tat	gag	ttg	gca	tac	ata	gaa	ccc	aaa	gga	agg	1407	
Ser	Ser	Ser	Ile	Trp	Tyr	Glu	Leu	Ala	Tyr	Ile	Glu	Pro	Lys	Gly	Arg		
				430				435						440			
atg	aag	aaa	ggc	aat	aaa	gtt	tgg	cag	att	gct	tta	ggg	tca	ggc	ttt	1455	
Met	Lys	Lys	Gly	Asn	Lys	Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe		
			445					450				455					
aag	tgt	aac	agt	gca	gtt	tgg	gtg	gct	cta	aac	aat	gtc	aaa	gct	tca	1503	
Lys	Cys	Asn	Ser	Ala	Val	Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser		

460	465	470	
aca aat agt cct tgg gaa cac tgc atc gac aga tac ccg gtt aaa att			1551
Thr Asn Ser Pro Trp Glu His Cys Ile Asp Arg Tyr Pro Val Lys Ile			
475	480	485	
gat tct gat tca ggt aag tca gag act cgt gtc cca aac ggt cgg tcc			1599
Asp Ser Asp Ser Gly Lys Ser Glu Thr Arg Val Pro Asn Gly Arg Ser			
490	495	500	505
taataaatga tgtttgctct ctttcgtttc tttttattgg ttataataat ttgatggcca			1659
cgatgtttct cttgtttgtt atgaataaag aatcccacgg tgttctagta aaaaaaaaaa			1719
aaaaaaaaaa aaaaaaa			1736

<210> 6

<211> 505

<212> PRT

<213> Brassica napus

<400> 6

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Ala Tyr Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr Leu	
35 40 45	
Gln His Asn Leu Ile Thr Ile Ala Pro Leu Leu Ala Phe Thr Val Phe	
50 55 60	
Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu Val	
65 70 75 80	
Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser	
85 90 95	
Lys Val Met Asp Ile Phe Phe Gln Val Arg Lys Ala Asp Pro Ser Arg	
100 105 110	
Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile	
115 120 125	
Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu	
130 135 140	
Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Arg Ala Arg Glu Glu Thr	
145 150 155 160	
Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn	
165 170 175	
Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe	
180 185 190	
Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu	
195 200 205	
Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala	
210 215 220	
Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys	
225 230 235 240	
Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile	
245 250 255	
Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg	
260 265 270	
Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Arg Asp Arg Arg	
275 280 285	
Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala	

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      290                      295                      300
Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn Gly
305                      310                      315                      320
Gln Thr Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg
      325                      330                      335
Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu
      340                      345                      350
Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe
      355                      360                      365
Lys Asp Glu Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile
      370                      375                      380
Asp His Phe Cys Ile His Ala Gly Gly Lys Ala Val Ile Asp Val Leu
385                      390                      395                      400
Glu Lys Asn Leu Gly Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser
      405                      410                      415
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu
      420                      425                      430
Leu Ala Tyr Ile Glu Pro Lys Gly Arg Met Lys Lys Gly Asn Lys Val
      435                      440                      445
Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp
450                      455                      460
Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His
465                      470                      475                      480
Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser
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Glu Thr Arg Val Pro Asn Gly Arg Ser
      500                      505

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<210> 7

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from *A. thaliana* FAE1 (SEQ ID NO:1) and
 3' 1179 bp from *B. napus* elongase KCS (SEQ ID
 NO:3); designated At114

<221> CDS

<222> (1)...(1518)

<400> 7

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ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa      96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
      20                      25                      30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
      35                      40                      45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc      192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
      50                      55                      60

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ggt ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt ccg cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc ccg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	

aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg	1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395 400	
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gag ttg gca tac ata gaa rca aaa gga agg atg aag aaa ggt aat aaa	1344
Glu Leu Ala Tyr Ile Glu Xaa Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt	1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa	1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu	
465 470 475 480	
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys	
485 490 495	
tca gag act cgt gtc cca aac ggt cgg tcc taa	1521
Ser Glu Thr Arg Val Pro Asn Gly Arg Ser	
500 505	

<210> 8
 <211> 506
 <212> PRT
 <213> Artificial Sequence

<220>

<221> VARIANT

<222> (0)...(0)

<223> Xaa = Ala or Thr

<223> 5' 114 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 392 amino acids from *B. napus* elongase KCS (SEQ ID NO:4); designated At114

<400> 8

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		20						25				30			
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
		35					40					45			
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
	50					55					60				
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val
65				70					75					80	
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser
				85					90					95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser
			100					105					110		
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys
		115					120					125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly
	130					135					140				
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu
145					150				155					160	
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
			165					170						175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
		180					185						190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
	195						200					205			
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210					215					220				
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225					230				235					240	
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
			245						250					255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
		260					265						270		
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg
		275					280					285			
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
	290					295					300				
Ala	Asp	Gly	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn
305					310				315					320	
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly
			325					330						335	

Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Xaa Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
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 485 490 495
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 500 505

<210> 9

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 222 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1296 bp from B. napus elongase KCS (SEQ ID
 NO:3); designated At74

<221> CDS

<222> (1)...(1515)

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ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aaa ccg gtt tac ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val	
65 70 75 80	

gag	tac	tca	tgc	tac	ctt	cca	cca	acg	cat	tgt	aga	tca	agt	atc	tcc	288
Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile	Ser	
				85					90					95		
aag	gtc	atg	gat	atc	ttt	tat	caa	gta	aga	aaa	gct	gat	cct	tct	cgg	336
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser	Arg	
				100					105					110		
aac	ggc	acg	tgc	gat	gac	tcg	tcg	tgg	ctt	gac	ttc	ttg	agg	aag	att	384
Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	Ile	
				115					120					125		
caa	gaa	cgt	tca	ggg	cta	ggc	gat	gaa	act	cac	ggg	ccc	gag	ggg	ctg	432
Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	Leu	
				130					135					140		
ctt	cag	gtc	cct	ccc	cgg	aag	act	ttt	gcg	gcg	gcg	cgt	gaa	gag	acg	480
Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	Thr	
				145					150					155		
gag	caa	gtt	atc	att	ggg	gag	cta	gaa	aat	cta	ttc	aag	aac	acc	aac	528
Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	Asn	
				165					170					175		
gtt	aac	cct	aaa	gat	ata	ggg	ata	ctt	gtg	gtg	aac	tca	agc	atg	ttt	576
Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	Phe	
				180					185					190		
aat	cca	act	cca	tcg	ctc	tcc	gag	atg	gtc	gtt	aac	act	ttc	aag	ctc	624
Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	Leu	
				195					200					205		
cga	agc	aac	gta	aga	agc	ttt	aac	ctt	ggg	ggc	atg	ggg	tgt	agt	gcc	672
Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	
				210					215					220		
ggc	gtt	ata	gcc	att	gat	cta	gca	aag	gac	ttg	ttg	cat	gtc	cat	aaa	720
Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	Lys	
				225					230					235		
aat	acg	tat	gct	ctt	gtg	gtg	agc	aca	gag	aac	atc	act	tat	aac	att	768
Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	Ile	
				245					250					255		
tac	gct	ggg	gat	aat	agg	tcc	atg	atg	gtt	tca	aat	tgc	ttg	ttc	cgt	816
Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	Arg	
				260					265					270		
gtt	ggg	ggg	gcc	gct	att	ttg	ctc	tcc	aac	aag	cct	gga	gat	cgt	aga	864
Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	Arg	
				275					280					285		
cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	gtt	cga	acg	cat	acc	gga	gct	912
Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	Ala	
				290					295					300		
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<210> 10
<211> 505
<212> PRT
<213> Artificial Sequence
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<220>

<223> 5' 74 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 431 amino acids from *B. napus* elongase KCS (SEQ ID NO:4); designated At74

<400> 10

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn
1				5					10					15	
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys
		20						25				30			
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu
		35					40				45				
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe
	50					55					60				
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu	Val
65					70					75					80
Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile	Ser
				85					90					95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser	Arg
			100					105					110		
Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	Ile
		115					120					125			
Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	Leu
	130					135					140				
Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	Thr
145					150					155					160
Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	Asn
				165					170					175	
Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	Phe
			180					185					190		
Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	Leu
		195					200					205			
Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala
		210				215					220				
Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	Lys
225				230						235					240
Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	Ile
			245						250					255	
Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	Arg
		260					265						270		
Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	Arg
		275					280					285			
Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	Ala
					290		295				300				
Asp	Gly	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	Gly
305					310					315					320
Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	Arg
			325						330					335	
Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	Leu
			340					345					350		
Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	Phe
		355					360					365			
Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	Ile
	370					375					380				
Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	Leu
385					390					395					400
Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	Ser

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          405          410          415
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu
          420          425          430
Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val
          435          440          445
Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp
          450          455          460
Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His
          465          470          475          480
Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser
          485          490          495
Glu Thr Arg Val Gln Asn Gly Arg Ser
          500          505

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<210> 11

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1179 bp from B. napus elongase KCS (SEQ ID
 NO:3) having mutations at positions 271, 272 and
 275; designated At114 L91C K92R

<221> CDS

<222> (1)...(1518)

<400> 11

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atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac      48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
  1              5              10              15

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ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa      96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
          20              25              30

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gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
          35              40              45

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caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc      192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
          50              55              60

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ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt      240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
          65              70              75              80

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gac tac tcg tgt tac ctt ccg cca ccg cat tgc aga gtt agt gtc tct      288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Cys Arg Val Ser Val Ser
          85              90              95

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aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca      336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
          100              105              110

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cgg aac ggc acg tgt gat aat tcg tcg tgg ctt gac ttc ttg agg aag Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys 115 120 125	384
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly 130 135 140	432
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu 145 150 155 160	480
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr 165 170 175	528
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met 180 185 190	576
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 195 200 205	624
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 210 215 220	672
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 225 230 235 240	720
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn 245 250 255	768
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 270	816
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 275 280 285	864
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 290 295 300	912
gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 305 310 315 320	960
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325 330 335	1008
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056

Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg	1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395 400	
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt	1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa	1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu	
465 470 475 480	
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys	
485 490 495	
tca gag act cgt gtc cca aac ggt cgg tcc taa	1521
Ser Glu Thr Arg Val Pro Asn Gly Arg Ser	
500 505	

<210> 12

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 392 amino acids from B. napus elongase KCS (SEQ ID NO:4) having mutations at residues 91 and 92; designated At114 L91C K92R

<400> 12

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn

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1	5	10	15
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys			
20	25	30	
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu			
35	40	45	
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe			
50	55	60	
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val			
65	70	75	80
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Cys Arg Val Ser Val Ser			
85	90	95	
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser			
100	105	110	
Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys			
115	120	125	
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly			
130	135	140	
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu			
145	150	155	160
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr			
165	170	175	
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met			
180	185	190	
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			
195	200	205	
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			
210	215	220	
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			
225	230	235	240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn			
245	250	255	
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
260	265	270	
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg			
275	280	285	
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly			
290	295	300	
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn			
305	310	315	320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly			
325	330	335	
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro			
340	345	350	
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu			
355	360	365	
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala			
370	375	380	
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val			
385	390	395	400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg			
405	410	415	
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr			
420	425	430	
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys			
435	440	445	
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val			
450	455	460	

Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 500 505

<210> 13

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from *A. thaliana* FAE1 (SEQ ID NO:1) and
 3' 1179 bp from *B. napus* elongase KCS (SEQ ID
 NO:3), having a mutation at position 275;
 designated At114 K92R

<221> CDS

<222> (1)...(1518)

<400> 13

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac 48
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60

ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt 240
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80

gac tac tcg tgt tac ctt ccg cca ccg cat ctc aga gtt agt gtc tct 288
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser
 85 90 95

aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca 336
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110

cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag 384
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125

att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg 432
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140

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ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	

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ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct    1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
  370                      375                      380

att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg    1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
  385                      390                      395                      400

cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga    1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
                      405                      410                      415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat    1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
                      420                      425                      430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa    1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
  435                      440                      445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt    1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
  450                      455                      460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa    1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
  465                      470                      475                      480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag    1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
                      485                      490                      495

tca gag act cgt gtc cca aac ggt cgg tcc taa    1521
Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
  500                      505

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<210> 14

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 392 amino acids from *B. napus* elongase KCS (SEQ ID NO:4), having a mutation at position 92; designated At114 K92R

<400> 14

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Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
  1           5           10           15
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
          20           25           30
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
          35           40           45
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
          50           55           60

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Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	65	70	75	80
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Arg	Val	Ser	Val	Ser	85	90	95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	100	105	110	
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	115	120	125	
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	130	135	140	
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	145	150	155	160
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	165	170	175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	180	185	190	
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	195	200	205	
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	210	215	220	
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	225	230	235	240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	245	250	255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	260	265	270	
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	275	280	285	
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	290	295	300	
Ala	Asp	Gly	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	305	310	315	320
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	325	330	335	
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	340	345	350	
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	355	360	365	
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	370	375	380	
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	385	390	395	400
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	405	410	415	
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	420	425	430	
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	435	440	445	
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	450	455	460	
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu	465	470	475	480
His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Ile	Asp	Ser	Asp	Ser	Gly	Lys	485	490	495	
Ser	Glu	Thr	Arg	Val	Pro	Asn	Gly	Arg	Ser							500	505		

<210> 15
 <211> 1521
 <212> DNA
 <213> Artificial Sequence

<220>

<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1179 bp from B. napus elongase KCS (SEQ ID
 NO:3), having a mutation at position 920;
 designated At114 G307D; hypothetical

<221> CDS

<222> (1)...(1518)

<400> 15

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	

ggc ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	

gac tac tcg tgt tac ctt ccg cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	

aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	

cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	

att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	

ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	

acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	

165	170	175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg			576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met			
180	185	190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag			624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			
195	200	205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt			672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			
210	215	220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat			720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			
225	230	235	240
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac			768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn			
245	250	255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc			816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
260	265	270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt			864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg			
275	280	285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga			912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly			
290	295	300	
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac			960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn			
305	310	315	320
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt			1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly			
325	330	335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg			1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro			
340	345	350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt			1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu			
355	360	365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct			1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala			
370	375	380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg			1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val			
385	390	395	400

cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga 1248
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat 1296
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa 1440
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495

tca gag act cgt gtc caa aac ggt cgg tcc taa 1521
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 16

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID
 NO:2) and 3' 392 amino acids from B. napus
 elongase KCS (SEQ ID NO:4) having mutation at
 residue 307; designated At114 G307D; hypothetical

<400> 16

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
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 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys

115	120	125
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly		
130	135	140
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu		
145	150	155
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr		
165	170	175
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met		
180	185	190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys		
195	200	205
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser		
210	215	220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His		
225	230	235
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn		
245	250	255
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe		
260	265	270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg		
275	280	285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly		
290	295	300
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn		
305	310	315
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly		
325	330	335
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro		
340	345	350
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu		
355	360	365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala		
370	375	380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val		
385	390	395
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg		
405	410	415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr		
420	425	430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys		
435	440	445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val		
450	455	460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu		
465	470	475
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys		
485	490	495
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser		
500	505	

<210> 17

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 222 bp from A. thaliana FAE1 (SEQ ID NO:1) and

3' 1296 bp from B. napus elongase KCS (SEQ ID
NO:3) having a mutation at position 917;
designated At74 G306D; hypothetical

<221> CDS

<222> (1)...(1515)

<400> 17

atg	acg	tcc	ggt	aac	ggt	aag	ctc	ctt	tac	cgt	tac	gtc	tta	acc	aac	48
Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn	
1				5					10					15		

ttt	ttc	aac	ctc	tgt	ttg	ttc	ccg	tta	acg	gcg	ttc	ctc	gcc	gga	aaa	96
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	
			20					25					30			

gcc	tct	cgg	ctt	acc	ata	aac	gat	ctc	cac	aac	ttc	ctt	tcc	tat	ctc	144
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	
			35				40					45				

caa	cac	aac	ctt	ata	aca	gta	act	tta	ctc	ttt	gct	ttc	act	ggt	ttc	192
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	
		50				55					60					

ggt	ttg	ggt	ctc	tac	atc	gta	acc	cga	ccc	aaa	ccg	ggt	tac	ctc	ggt	240
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu	Val	
65					70					75				80		

gag	tac	tca	tgc	tac	ctt	cca	cca	acg	cat	tgt	aga	tca	agt	atc	tcc	288
Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile	Ser	
				85				90						95		

aag	gtc	atg	gat	atc	ttt	tat	caa	gta	aga	aaa	gct	gat	cct	tct	cgg	336
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser	Arg	
			100					105					110			

aac	ggc	acg	tgc	gat	gac	tcg	tcg	tgg	ctt	gac	ttc	ttg	agg	aag	att	384
Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	Ile	
		115					120					125				

caa	gaa	cgt	tca	ggt	cta	ggc	gat	gaa	act	cac	ggg	ccc	gag	ggg	ctg	432
Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	Leu	
		130				135					140					

ctt	cag	gtc	cct	ccc	cgg	aag	act	ttt	gcg	gcg	gcg	cgt	gaa	gag	acg	480
Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	Thr	
145					150					155				160		

gag	caa	ggt	atc	att	ggt	gcg	cta	gaa	aat	cta	ttc	aag	aac	acc	aac	528
Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	Asn	
			165					170					175			

ggt	aac	cct	aaa	gat	ata	ggt	ata	ctt	gtg	gtg	aac	tca	agc	atg	ttt	576
Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	Phe	
			180					185					190			

aat	cca	act	cca	tcg	ctc	tcc	gcg	atg	gtc	ggt	aac	act	ttc	aag	ctc	624
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	Leu	
	195						200					205				
cga	agc	aac	gta	aga	agc	ttt	aac	ctt	ggg	ggc	atg	ggg	tgt	agt	gcc	672
Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	Ala	
	210					215					220					
ggc	gtt	ata	gcc	att	gat	cta	gca	aag	gac	ttg	ttg	cat	gtc	cat	aaa	720
Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	Lys	
	225				230					235					240	
aat	acg	tat	gct	ctt	gtg	gtg	agc	aca	gag	aac	atc	act	tat	aac	att	768
Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	Ile	
				245					250					255		
tac	gct	ggg	gat	aat	agg	tcc	atg	atg	gtt	tca	aat	tgc	ttg	ttc	cgt	816
Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	Arg	
			260					265					270			
gtt	ggg	ggg	gcc	gct	att	ttg	ctc	tcc	aac	aag	cct	gga	gat	cgt	aga	864
Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	Arg	
			275				280					285				
cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	gtt	cga	acg	cat	acc	gga	gct	912
Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	Ala	
	290					295					300					
gac	gac	aag	tct	ttt	cgt	tgc	gtg	caa	caa	gga	gac	gat	gag	aac	ggc	960
Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	Gly	
	305				310					315					320	
aaa	atc	gga	gtg	agt	ttg	tcc	aag	gac	ata	acc	gat	gtt	gct	ggg	cga	1008
Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	Arg	
				325				330						335		
acg	gtt	aag	aaa	aac	ata	gca	acg	ttg	ggg	ccg	ttg	att	ctt	ccg	tta	1056
Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	Leu	
			340					345					350			
agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	ttc	atg	ggc	aag	aaa	ctt	ttc	1104
Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	Phe	
		355					360					365				
aaa	gat	aaa	atc	aaa	cat	tac	tac	gtc	ccg	gat	ttc	aaa	ctt	gct	att	1152
Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	Ile	
	370					375					380					
gac	cat	ttt	tgt	ata	cat	gcc	gga	ggc	aga	gcc	gtg	att	gat	gtg	cta	1200
Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	Leu	
	385				390				395						400	
gag	aag	aac	cta	gcc	cta	gca	ccg	atc	gat	gta	gag	gca	tca	aga	tca	1248
Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	Ser	
			405					410					415			
acg	tta	cat	aga	ttt	gga	aac	act	tca	tct	agc	tca	ata	tgg	tat	gag	1296
Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	Glu	

420	425	430	
ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa gtt			1344
Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val			
435	440	445	
tggtg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt tgg			1392
Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp			
450	455	460	
gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa cac			1440
Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His			
465	470	475	480
tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag tca			1488
Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser			
485	490	495	
gag act cgt gtc caa aac ggt cgg tcc taa			1518
Glu Thr Arg Val Gln Asn Gly Arg Ser			
500	505		

<210> 18

<211> 505

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 74 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 431 amino acids from B. napus elongase KCS (SEQ ID NO:4) having a mutation at residue 306; designated At74 G306D; hypothetical

<400> 18

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn			
1	5	10	15
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys			
20	25	30	
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu			
35	40	45	
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe			
50	55	60	
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Lys Pro Val Tyr Leu Val			
65	70	75	80
Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile Ser			
85	90	95	
Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser Arg			
100	105	110	
Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys Ile			
115	120	125	
Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly Leu			
130	135	140	
Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu Thr			
145	150	155	160
Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr Asn			
165	170	175	

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Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met Phe
      180                      185                      190
Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys Leu
      195                      200                      205
Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser Ala
      210                      215                      220
Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His Lys
      225                      230                      235                      240
Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn Ile
      245                      250                      255
Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe Arg
      260                      265                      270
Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg Arg
      275                      280                      285
Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly Ala
      290                      295                      300
Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn Gly
      305                      310                      315                      320
Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly Arg
      325                      330                      335
Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro Leu
      340                      345                      350
Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu Phe
      355                      360                      365
Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala Ile
      370                      375                      380
Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val Leu
      385                      390                      395                      400
Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg Ser
      405                      410                      415
Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr Glu
      420                      425                      430
Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys Val
      435                      440                      445
Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val Trp
      450                      455                      460
Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu His
      465                      470                      475                      480
Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys Ser
      485                      490                      495
Glu Thr Arg Val Gln Asn Gly Arg Ser
      500                      505

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<210> 19

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1179 bp from B. napus elongase KCS (SEQ ID
 NO:3) having mutations at positions 271, 272, 275
 and 920; designated At114 L91C K92R G307D;
 hypothetical

<221> CDS

<222> (1)...(1518)

<400> 19

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tat gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt ccg cca ccg cat tgc aga gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Cys Arg Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac ggc acg tgt gat aat tcg tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	

gcc Ala 225	ggc Gly	gtt Val	ata Ile	gcc Ala	att Ile 230	gat Asp	cta Leu	gca Ala	aag Lys	gac Asp 235	ttg Leu	ttg Leu	cat His	gtc Val	cat His 240	720
aaa Lys	aat Asn	acg Thr	tat Tyr 245	gct Ala	ctt Leu	gtg Val	gtg Val	agc Ser	aca Thr 250	gag Glu	aac Asn	atc Ile	act Thr	tat Tyr 255	aac Asn	768
att Ile	tac Tyr	gct Ala	ggt Gly 260	gat Asp	aat Asn	agg Arg	tcc Ser	atg Met 265	atg Met	gtt Val	tca Ser	aat Asn	tgc Cys 270	ttg Leu	ttc Phe	816
cgt Arg	gtt Val	ggg Gly 275	ggg Gly	gcc Ala	gct Ala	att Ile 280	ttg Leu	ctc Leu	tcc Ser	aac Asn	aag Lys 285	cct Pro	gga Gly	gat Asp	cgt Arg	864
aga Arg 290	cgg Arg	tcc Ser	aag Lys	tac Tyr	gag Glu	cta Leu 295	gtt Val	cac His	acg Thr	gtt Val	cga Arg 300	acg Thr	cat His	acc Thr	gga Gly	912
gct Ala 305	gac Asp	gac Asp	aag Lys	tct Ser	ttt Phe 310	cgt Arg	tgc Cys	gtg Val	caa Gln	caa Gln 315	gga Gly	gac Asp	gat Asp	gag Glu	aac Asn 320	960
ggc Gly	aaa Lys	atc Ile	gga Gly 325	gtg Val	agt Ser	ttg Leu	tcc Ser	aag Lys 330	gac Asp	ata Ile	acc Thr	gat Asp	gtt Val	gct Ala 335	ggg Gly	1008
cga Arg	acg Thr	gtt Val	aag Lys 340	aaa Lys	aac Asn	ata Ile	gca Ala	acg Thr 345	ttg Leu	ggg Gly	ccg Pro	ttg Leu	att Ile 350	ctt Leu	ccg Pro	1056
tta Leu	agc Ser	gag Glu 355	aaa Lys	ctt Leu	ctt Leu	ttt Phe	ttc Phe 360	gtt Val	acc Thr	ttc Phe	atg Met 365	ggc Gly	aag Lys	aaa Lys	ctt Leu	1104
ttc Phe 370	aaa Lys	gat Asp	aaa Lys	atc Ile	aaa Lys	cat His 375	tac Tyr	tac Tyr	gtc Val	ccg Pro	gat Asp 380	ttc Phe	aaa Lys	ctt Leu	gct Ala	1152
att Ile 385	gac Asp	cat His	ttt Phe	tgt Cys	ata Ile 390	cat His	gcc Ala	gga Gly	ggc Gly	aga Arg 395	gcc Ala	gtg Val	att Ile	gat Asp	gtg Val 400	1200
cta Leu	gag Glu	aag Lys	aac Asn 405	cta Leu	gcc Ala	cta Leu	gca Ala	ccg Pro	atc Ile 410	gat Asp	gta Val	gag Glu	gca Ala	tca Ser	aga Arg 415	1248
tca Ser	acg Thr	tta Leu	cat His 420	aga Arg	ttt Phe	gga Gly	aac Asn	act Thr 425	tca Ser	tct Ser	agc Ser	tca Ser	ata Ile 430	tgg Trp	tat Tyr	1296
gag Glu	ttg Leu	gca Ala 435	tac Tyr	ata Ile	gaa Glu	gca Ala	aaa Lys 440	gga Gly	agg Arg	atg Met	aag Lys	aaa Lys 445	ggg Gly	aat Asn	aaa Lys	1344

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa 1440
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495

tca gag act cgt gtc caa aac ggt cgg tcc taa 1521
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 20

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID
 NO:2) and 3' 392 amino acids from B. napus
 elongase KCS (SEQ ID NO:4) having mutations at
 positions 91, 92 and 307; designated At114 L91C
 K92R G307D; hypothetical

<400> 20

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Cys Arg Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Gly Thr Cys Asp Asn Ser Ser Trp Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
 130 135 140
 Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu
 145 150 155 160
 Thr Glu Gln Val Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
 165 170 175
 Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser

210	215	220
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His		
225	230	235
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn		240
	245	250
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe		255
	260	265
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg		270
	275	280
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly		285
	290	295
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn		300
305	310	315
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly		320
	325	330
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro		335
	340	345
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu		350
	355	360
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala		365
370	375	380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val		385
385	390	395
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg		400
	405	410
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr		415
	420	425
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys		430
	435	440
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val		445
	450	455
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu		460
465	470	475
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys		480
	485	490
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser		495
	500	505

<210> 21

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 342 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1179 bp from B. napus elongase KCS (SEQ ID
 NO:3) having mutations at positions 275 and 920;
 designated At114 K92R G307D; hypothetical

<221> CDS

<222> (1)...(1518)

<400> 21

atg	acg	tcc	gtt	aac	gtt	aag	ctc	ctt	tac	cgt	tat	gtc	tta	acc	aac
Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn
1				5						10					15

48

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt ccg cca ccg cat ctc aga gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac ggc acg tgt gat gat tcg tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc ccg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768

Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn		
				245					250						255		
att	tac	gct	ggt	gat	aat	agg	tcc	atg	atg	gtt	tca	aat	tgc	ttg	ttc	816	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe		
			260					265					270				
cgt	gtt	ggt	ggg	gcc	gct	att	ttg	ctc	tcc	aac	aag	cct	gga	gat	cgt	864	
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg		
		275					280					285					
aga	cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	gtt	cga	acg	cat	acc	gga	912	
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly		
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gct	gac	gac	aag	tct	ttt	cgt	tgc	gtg	caa	caa	gga	gac	gat	gag	aac	960	
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn		
305					310				315						320		
ggc	aaa	atc	gga	gtg	agt	ttg	tcc	aag	gac	ata	acc	gat	gtt	gct	ggt	1008	
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly		
				325					330					335			
cga	acg	gtt	aag	aaa	aac	ata	gca	acg	ttg	ggt	ccg	ttg	att	ctt	ccg	1056	
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro		
			340					345					350				
tta	agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	ttc	atg	ggc	aag	aaa	ctt	1104	
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu		
		355					360					365					
ttc	aaa	gat	aaa	atc	aaa	cat	tac	tac	gtc	ccg	gat	ttc	aaa	ctt	gct	1152	
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala		
	370					375					380						
att	gac	cat	ttt	tgt	ata	cat	gcc	gga	ggc	aga	gcc	gtg	att	gat	gtg	1200	
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val		
385					390				395					400			
cta	gag	aag	aac	cta	gcc	cta	gca	ccg	atc	gat	gta	gag	gca	tca	aga	1248	
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg		
			405					410						415			
tca	acg	tta	cat	aga	ttt	gga	aac	act	tca	tct	agc	tca	ata	tgg	tat	1296	
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr		
			420					425					430				
gag	ttg	gca	tac	ata	gaa	gca	aaa	gga	agg	atg	aag	aaa	ggt	aat	aaa	1344	
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys		
		435					440					445					
gtt	tgg	cag	att	gct	tta	ggg	tca	ggc	ttt	aag	tgt	aac	agt	gca	gtt	1392	
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val		
	450					455					460						
tgg	gtg	gct	cta	aac	aat	gtc	aaa	gct	tcg	aca	aat	agt	cct	tgg	gaa	1440	
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu		

tca gag act cgt gtc caa aac ggt cgg tcc taa 1521
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
500 505

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<220>
<223> 5' 114 amino acids from A. thaliana FAE1 (SEQ ID
      NO:2) and 3' 392 amino acids from B. napus
      elongase KCS (SEQ ID NO:4) having mutations at
      positions 92 and 307; designated At114 K92R G307D;
      hypothetical
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<400> 22																
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			20					25					30			
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	
			35				40					45				
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	
			50			55					60					
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	
65					70					75					80	
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Arg	Val	Ser	Val	Ser	
			85						90					95		
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	
			100					105					110			
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	
			115				120						125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	
			130			135					140					
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu	
145					150					155					160	
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	
			165						170					175		
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	
			180				185						190			
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	
			195				200					205				
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	
			210			215					220					
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	
225					230					235					240	
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	
			245						250					255		
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	

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      260      265      270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg
      275      280      285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
      290      295      300
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
305      310      315      320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
      325      330      335
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
      340      345      350
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
      355      360      365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
      370      375      380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
385      390      395      400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
      405      410      415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
      420      425      430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
      435      440      445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
      450      455      460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
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His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
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Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
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<210> 23

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 762 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 759 bp from B. napus elongase KCS (SEQ ID
 NO:3); designated At254

<221> CDS

<222> (1)...(1518)

<400> 23

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  1              5              10              15

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ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa      96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
      20              25              30

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gcc tct cgg ctt acc ata aac gat ctc cac aac ctc ctt tcc tat ctc      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Leu Leu Ser Tyr Leu
      35              40              45

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caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag	384
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly	
130 135 140	
ctc att cac gta cca ccg ccg aag act ttt gca gcg tca cgt gaa gag	480
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu	
145 150 155 160	
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc gag aac acc	528
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr	
165 170 175	
aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg	576
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt	672
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aac act tat gct ctc gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	

cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960
Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg	1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395 400	
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr	
420 425 430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt	1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa	1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu	
465 470 475 480	
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys	
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500 505

<210> 24

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 254 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 252 amino acids from *B. napus* elongase KCS (SEQ ID NO:4); designated At254

<400> 24

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Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	20	25	30	
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Leu	Leu	Ser	Tyr	Leu	35	40	45	
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	50	55	60	
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	65	70	75	80
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser	85	90	95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	100	105	110	
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys	115	120	125	
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly	130	135	140	
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu	145	150	155	160
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Glu	Asn	Thr	165	170	175	
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	180	185	190	
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	195	200	205	
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	210	215	220	
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	225	230	235	240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	245	250	255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	260	265	270	
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	275	280	285	
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	290	295	300	
Ala	Asp	Gly	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	305	310	315	320
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	325	330	335	

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 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
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 Ser Glu Thr Arg Val Pro Asn Gly Arg Ser
 500 505

<210> 25

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 519 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 1002 bp from B. napus elongase KCS (SEQ ID
 NO:3); designated At173

<221> CDS

<222> (1)...(1518)

<400> 25

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ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	

gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag	384
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly	
130 135 140	
ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag	480
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu	
145 150 155 160	
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc aag aac acc	528
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc gcc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gac gcc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960

Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg	1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395 400	
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt	1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	
450 455 460	
tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa	1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu	
465 470 475 480	
cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys	
485 490 495	
tca gag act cgt gtc cma aac ggt cgg tcc taa	1521
Ser Glu Thr Arg Val Xaa Asn Gly Arg Ser	
500 505	

<210> 26

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 173 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 333 amino acids from *B. napus* elongase KCS (SEQ ID NO:4); designated At173

<221> VARIANT

<222> (0)...(0)

<223> Xaa = Pro or Gln

<400> 26

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn	1	5	10	15
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	20	25	30	
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	35	40	45	
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	50	55	60	
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	65	70	75	80
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser	85	90	95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	100	105	110	
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys	115	120	125	
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly	130	135	140	
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu	145	150	155	160
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	165	170	175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	180	185	190	
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	195	200	205	
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	210	215	220	
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	225	230	235	240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	245	250	255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	260	265	270	
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	275	280	285	
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	290	295	300	
Ala	Asp	Gly	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	305	310	315	320
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	325	330	335	
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	340	345	350	
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	355	360	365	
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala				

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      370              375              380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
385              390              395              400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
      405              410              415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
      420              425              430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
      435              440              445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
      450              455              460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465              470              475              480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
      485              490              495
Ser Glu Thr Arg Val Xaa Asn Gly Arg Ser
      500              505

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<210> 27

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 528 bp from *B. napus* elongase KCS (SEQ ID NO:3)
and 3' 993 bp from *A. thaliana* FAEl (SEQ ID NO:1);
designated Bn176

<221> CDS

<222> (1)...(1518)

<400> 27

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atg acg tcc att aac gta aag ctc ctt tac cat tac gtc ata acc aac      48
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
  1              5              10              15

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```

ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa      96
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
      20              25              30

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```

gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat      144
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
      35              40              45

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```

ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt      192
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
      50              55              60

```

```

ttc ggt tcg gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc      240
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
      65              70              75              80

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gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc      288
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
      85              90              95

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```

tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct      336

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Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser		
			100					105					110				
cgg	aac	ggc	acg	tgc	gat	gac	tcg	tcg	tgg	ctt	gac	ttc	ttg	agg	aag	384	
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys		
		115					120					125					
att	caa	gaa	cgt	tca	ggg	cta	ggc	gat	gaa	act	cac	ggg	ccc	gag	ggg	432	
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly		
	130					135					140						
ctg	ctt	cag	gtc	cct	ccc	cgg	aag	act	ttt	gcg	gcg	gcg	cgt	gaa	gag	480	
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu		
145					150					155					160		
acg	gag	caa	gtt	atc	att	ggg	gcg	cta	gaa	aat	cta	ttc	aag	aac	acc	528	
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr		
			165					170					175				
aaa	gtt	aac	cct	aga	gag	att	ggg	ata	ctt	gtg	gtg	aac	tca	agc	atg	576	
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met		
			180				185						190				
ttt	aat	cca	act	cct	tcg	cta	tcc	gct	atg	gtc	gtt	aat	act	ttc	aag	624	
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys		
		195					200						205				
ctc	cga	agc	aac	atc	aaa	agc	ttt	aat	cta	gga	gga	atg	ggg	tgt	agt	672	
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser		
	210					215						220					
gct	ggg	gtt	att	gcc	att	gat	ttg	gct	aaa	gac	ttg	ttg	cat	gtt	cat	720	
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His		
225					230					235					240		
aaa	aac	act	tat	gct	ctt	gtg	gtg	agc	act	gag	aac	atc	aca	caa	ggc	768	
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Gln	Gly		
				245					250					255			
att	tat	gct	gga	gaa	aat	aga	tca	atg	atg	gtt	agc	aat	tgc	ttg	ttt	816	
Ile	Tyr	Ala	Gly	Glu	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe		
			260					265					270				
cgt	gtt	ggg	ggg	gcc	gcg	att	ttg	ctc	tct	aac	aag	tcg	gga	gac	cgg	864	
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Ser	Gly	Asp	Arg		
		275					280						285				
aga	cgg	tcc	aag	tac	aag	cta	gtt	cac	acg	gtc	cga	acg	cat	act	gga	912	
Arg	Arg	Ser	Lys	Tyr	Lys	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly		
		290				295					300						
gct	gat	gac	aag	tct	ttt	cga	tgt	gtg	caa	caa	gaa	gat	gat	gag	agc	960	
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Glu	Asp	Asp	Glu	Ser		
305					310					315					320		
ggc	aaa	atc	gga	gtt	tgt	ctg	tca	aag	gac	ata	acc	aat	gtt	gcg	ggg	1008	
Gly	Lys	Ile	Gly	Val	Cys	Leu	Ser	Lys	Asp	Ile	Thr	Asn	Val	Ala	Gly		

	325	330	335	
aca aca ctt acg aaa aat ata gca aca ttg ggt ccg ttg att ctt cct				1056
Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro				
	340	345	350	
tta agc gaa aag ttt ctt ttt ttc gct acc ttc gtc gcc aag aaa ctt				1104
Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu				
	355	360	365	
cta aag gat aaa atc aag cat tac tat gtt ccg gat ttc aag ctt gct				1152
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala				
	370	375	380	
gtt gac cat ttc tgt att cat gcc gga ggc aga gcc gtg atc gat gag				1200
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu				
	385	390	395	400
cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga				1248
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg				
	405	410	415	
tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat				1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ile Trp Tyr				
	420	425	430	
gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa				1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys				
	435	440	445	
gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt				1392
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val				
	450	455	460	
tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa				1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln				
	465	470	475	480
cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag				1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys				
	485	490	495	
tca aag act cat gtc caa aac ggt cgg tcc taa				1521
Ser Lys Thr His Val Gln Asn Gly Arg Ser				
	500	505		

<210> 28

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 176 amino acids from B. napus elongase KCS (SEQ
ID NO:4) and 3' 330 amino acids from A. thaliana
FAE1 (SEQ ID NO:2); designated Bn176

<400> 28

Met	Thr	Ser	Ile	Asn	Val	Lys	Leu	Leu	Tyr	His	Tyr	Val	Ile	Thr	Asn
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Leu	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	Thr	Ala	Ile	Val	Ala	Gly	Lys
		20						25					30		
Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	Ser	Tyr
		35					40					45			
Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	Thr	Val
	50					55					60				
Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu
65					70				75						80
Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile
				85					90					95	
Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser
			100					105					110		
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys
		115					120					125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly
	130				135						140				
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu
145					150					155					160
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
			165					170						175	
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
		180						185					190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
	195						200					205			
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210				215						220				
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225					230					235					240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Gln	Gly
				245					250					255	
Ile	Tyr	Ala	Gly	Glu	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
		260					265						270		
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Ser	Asn	Lys	Ser	Gly	Asp	Arg	
	275						280					285			
Arg	Arg	Ser	Lys	Tyr	Lys	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
	290					295					300				
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Glu	Asp	Asp	Glu	Ser
305					310					315					320
Gly	Lys	Ile	Gly	Val	Cys	Leu	Ser	Lys	Asp	Ile	Thr	Asn	Val	Ala	Gly
				325					330					335	
Thr	Thr	Leu	Thr	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro
		340						345					350		
Leu	Ser	Glu	Lys	Phe	Leu	Phe	Phe	Ala	Thr	Phe	Val	Ala	Lys	Lys	Leu
		355					360					365			
Leu	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala
	370					375					380				
Val	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Glu
385					390					395					400
Leu	Glu	Lys	Asn	Leu	Gly	Leu	Ser	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg
			405						410					415	
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr
			420					425					430		
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys
		435					440						445		

Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
 485 490 495
 Ser Lys Thr His Val Gln Asn Gly Arg Ser
 500 505

<210> 29

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 1197 bp from A. thaliana FAE1 (SEQ ID NO:1) and
 3' 324 bp from B. napus elongase KCS (SEQ ID
 NO:3); designated At399

<221> CDS

<222> (1)...(1518)

<400> 29

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac 48
 Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa 96
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc 144
 Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc 192
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60

ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt 240
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80

gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct 288
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95

aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca 336
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110

cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag 384
 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
 115 120 125

att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga 432
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly

130	135	140	
ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag			480
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu			
145	150	155 160	
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc gag aac acc			528
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr			
165	170	175	
aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg			576
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met			
180	185	190	
ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag			624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys			
195	200	205	
ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt			672
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser			
210	215	220	
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat			720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His			
225	230	235 240	
aaa aac act tat gct ctt gtg gtg agc act gag aac atc aca caa ggc			768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly			
245	250	255	
att tat gct gga gaa aat aga tca atg atg gtt agc aat tgc ttg ttt			816
Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe			
260	265	270	
cgt gtt ggt ggg gcc gcg att ttg ctc tct aac aag tcg gga gac cgg			864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg			
275	280	285	
aga cgg tcc aag tac aag cta gtt cac acg gtc cga acg cat act gga			912
Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly			
290	295	300	
gct gat gac aag tct ttt cga tgt gtg caa caa gaa gac gat gag agc			960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser			
305	310	315 320	
ggc aaa atc gga gtt tgt ctg tca aag gac ata acc aat gtt gcg ggg			1008
Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly			
325	330	335	
aca aca ctt acg aaa aat ata gca aca ttg ggt ccg ttg att ctt cct			1056
Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro			
340	345	350	
tta agc gaa aag ttt ctt ttt ttc gct acc ttc gtc gcc aag aaa ctt			1104
Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu			
355	360	365	

cta aag gat aaa atc aag cat tac tat gtt ccg gat ttc aag ctt gct 1152
 Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380

gtt gac cat ttc tgt att cat gcc gga ggc aga gcc gtg atc gat gtg 1200
 Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400

cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga 1248
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415

tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat 1296
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

tgg gtg gct cta aac aat gtc aaa gct tgc aca aat agt cct tgg gaa 1440
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495

tca gag act cgt gtc cma aac ggt cgg tcc taa 1521
 Ser Glu Thr Arg Val Xaa Asn Gly Arg Ser
 500 505

<210> 30

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 399 amino acids from A. thaliana FAE1 (SEQ ID
 NO:2) and 3' 107 amino acids from B. napus
 elongase KCS (SEQ ID NO:4); designated At399

<221> VARIANT

<222> (0)...(0)

<223> Xaa = Pro or Gln

<400> 30

Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1 5 10 15
 Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20 25 30

Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35 40 45
 Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
 50 55 60
 Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
 65 70 75 80
 Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser
 85 90 95
 Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
 100 105 110
 Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
 115 120 125
 Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
 130 135 140
 Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
 145 150 155 160
 Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr
 165 170 175
 Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
 180 185 190
 Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
 195 200 205
 Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
 210 215 220
 Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
 225 230 235 240
 Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly
 245 250 255
 Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
 260 265 270
 Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg
 275 280 285
 Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly
 290 295 300
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser
 305 310 315 320
 Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly
 325 330 335
 Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu
 355 360 365
 Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys

<400> 31																	
atg	acg	tcc	att	aac	gtt	aag	ctc	ctt	tac	cat	tac	gtc	ata	acc	aac	48	
Met	Thr	Ser	Ile	Asn	Val	Lys	Leu	Leu	Tyr	His	Tyr	Val	Ile	Thr	Asn		
1				5				10				15					
ctt	ttc	aac	ctt	tgc	ttc	ttt	ccg	tta	acg	gcg	atc	gtc	gcc	gga	aaa	96	
Leu	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	Thr	Ala	Ile	Val	Ala	Gly	Lys		
20				25				30									
gcc	tat	cgg	ctt	acc	ata	gac	gat	ctt	cac	cac	tta	tac	tat	tcc	tat	144	
Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	Ser	Tyr		
35				40				45									
ctc	caa	cac	aac	ctc	ata	acc	atc	gct	cca	ctc	ttt	gcc	ttc	acc	gtt	192	
Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	Thr	Val		
50				55				60									
ttc	ggg	tcg	gtt	ctc	tac	atc	gca	acc	cgg	ccc	aaa	ccg	gtt	tac	ctc	240	
Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu		
65				70				75				80					
gtt	gag	tac	tca	tgc	tac	ctt	cca	cca	acg	cat	tgt	aga	tca	agt	atc	288	
Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile		
85				90				95									
tcc	aag	gtc	atg	gat	atc	ttt	tat	caa	gta	aga	aaa	gct	gat	cct	tct	336	
Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser		
100				105				110									
cgg	aac	ggc	acg	tgc	gat	gac	tcg	tcg	tgg	ctt	gac	ttc	ttg	agg	aag	384	
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys		
115				120				125									
att	caa	gaa	cgt	tca	ggg	cta	ggc	gat	gaa	act	cac	ggg	ccc	gag	ggg	432	
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly		
130				135				140									
ctg	ctt	cag	gtc	cct	ccc	cgg	aag	act	ttt	gcg	gcg	gcg	cgt	gaa	gag	480	
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu		
145				150				155				160					

acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr 165 170 175	528
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met 180 185 190	576
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys 195 200 205	624
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser 210 215 220	672
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His 225 230 235 240	720
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn 245 250 255	768
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe 260 265 270	816
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg 275 280 285	864
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly 290 295 300	912
gct gac ggc aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn 305 310 315 320	960
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly 325 330 335	1008
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro 340 345 350	1056
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu 355 360 365	1104
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala 370 375 380	1152

att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg atc gat gag 1200
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
 385 390 395 400

cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga 1248
 Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415

tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat 1296
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430

gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt 1392
 Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa 1440
 Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
 465 470 475 480

cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
 485 490 495

tca aag act cat gtc caa aac ggt cgg tcc taa 1521
 Ser Lys Thr His Val Gln Asn Gly Arg Ser
 500 505

<210> 32

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 399 amino acids from B. napus elongase KCS (SEQ
 ID NO:3) and 3' 107 amino acids from A. thaliana
 FAEl (SEQ ID NO:1); designated Bn399

<400> 32

Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
 1 5 10 15
 Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
 20 25 30
 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
 35 40 45
 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
 50 55 60
 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
 65 70 75 80
 Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
 85 90 95
 Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser

	100		105		110
Arg	Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys				
	115		120		125
Ile	Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly				
	130		135		140
Leu	Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu				
145		150		155	160
Thr	Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr				
	165		170		175
Asn	Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met				
	180		185		190
Phe	Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys				
	195		200		205
Leu	Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser				
	210		215		220
Ala	Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His				
225		230		235	240
Lys	Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn				
	245		250		255
Ile	Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe				
	260		265		270
Arg	Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg				
	275		280		285
Arg	Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly				
	290		295		300
Ala	Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn				
305		310		315	320
Gly	Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly				
	325		330		335
Arg	Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro				
	340		345		350
Leu	Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu				
	355		360		365
Phe	Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala				
	370		375		380
Ile	Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu				
385		390		395	400
Leu	Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg				
	405		410		415
Ser	Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr				
	420		425		430
Glu	Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys				
	435		440		445
Ala	Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val				
	450		455		460
Trp	Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln				
465		470		475	480
His	Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys				
	485		490		495
Ser	Lys Thr His Val Gln Asn Gly Arg Ser				
	500		505		

<210> 33

<211> 1524

<212> DNA

<213> Artificial Sequence

<220>

<223> 1524 bp from B. napus elongase KCS (SEQ ID NO:3)
 having a mutation at position 920; designated Bn
 G307D; hypothetical

<221> CDS

<222> (1)...(1518)

<400> 33

atg acg tcc att aac gta aag ctc ctt tac cat tac gtc ata acc aac	48
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn	
1 5 10 15	
ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa	96
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys	
20 25 30	
gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat	144
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr	
35 40 45	
ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt	192
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val	
50 55 60	
ttc ggt tgc gtt ctc tac atc gca acc cgg ccc aaa ccg gtt tac ctc	240
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu	
65 70 75 80	
gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc	288
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile	
85 90 95	
tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct	336
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser	
100 105 110	
cgg aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	

ttt aat cca act cca tcc ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac	960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn	
305 310 315 320	
ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt	1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly	
325 330 335	
cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg	1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt	1104
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu	
355 360 365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct	1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg att gat gtg	1200
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val	
385 390 395 400	
cta gag aag aac cta gcc cta gca ccg atc gat gta gag gca tca aga	1248
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt gga aac act tca tct agc tca ata tgg tat	1296

Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
420 425 430

gag ttg gca tac ata gaa gca aaa gga agg atg aag aaa ggt aat aaa 1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
435 440 445

gtt tgg cag att gct tta ggg tca ggc ttt aag tgt aac agt gca gtt 1392
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
450 455 460

tgg gtg gct cta aac aat gtc aaa gct tcg aca aat agt cct tgg gaa 1440
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465 470 475 480

cac tgc atc gac aga tac ccg gtc aaa att gat tct gat tca ggt aag 1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
485 490 495

tca gag act cgt gtc caa aac ggt cgg tcc taataa 1524
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
500 505

<210> 34
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> 506 amino acids from B. napus elongase KCS (SEQ ID
NO:4) having a mutation at residue 307; designated
Bn G307D; hypothetical

<400> 34
Met Thr Ser Ile Asn Val Lys Leu Leu Tyr His Tyr Val Ile Thr Asn
1 5 10 15
Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
20 25 30
Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
35 40 45
Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
50 55 60
Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
65 70 75 80
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile
85 90 95
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser
100 105 110
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys
115 120 125
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly
130 135 140
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Arg Glu Glu
145 150 155 160
Thr Glu Gln Val Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr
165 170 175

Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	
			180					185					190			
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	
		195					200					205				
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	
	210					215					220					
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	
225					230					235					240	
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	
				245					250					255		
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	
			260					265					270			
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	
		275					280					285				
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	
	290					295					300					
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	
305					310					315					320	
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	
			325						330					335		
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	
		340						345					350			
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	
		355					360					365				
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	
	370					375					380					
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	
385					390					395					400	
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	
			405						410					415		
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	
		420						425					430			
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	
		435					440					445				
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	
	450					455					460					
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu	
465					470					475					480	
His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Ile	Asp	Ser	Asp	Ser	Gly	Lys	
			485						490					495		
Ser	Glu	Thr	Arg	Val	Gln	Asn	Gly	Arg	Ser							
			500					505								

<210> 35

<211> 1709

<212> DNA

<213> Artificial Sequence

<220>

<223> 1709 bp from A. thaliana FAE1 (SEQ ID NO:1) having
a mutation at position 275; designated At K92R;
hypothetical

<221> CDS

<222> (1)...(1518)

<400> 35

atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac	48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn	
1 5 10 15	
ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa	96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	
gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	
caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
50 55 60	
ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
65 70 75 80	
gac tac tcg tgt tac ctt cca cca ccg cat ctc aga gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser	
85 90 95	
aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag	384
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly	
130 135 140	
ctc att cac gta cca ccg cgg aag act ttt gca gcg tca cgt gaa gag	480
Leu Ile His Val Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu	
145 150 155 160	
aca gag aag gtt atc atc ggt gcg ctc gaa aat cta ttc gag aac acc	528
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr	
165 170 175	
aaa gtt aac cct aga gag att ggt ata ctt gtg gtg aac tca agc atg	576
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cct tcg cta tcc gct atg gtc gtt aat act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac atc aaa agc ttt aat cta gga gga atg ggt tgt agt	672
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gct ggt gtt att gcc att gat ttg gct aaa gac ttg ttg cat gtt cat	720

Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aac act tat gct ctt gtg gtg agc act gag aac atc aca caa ggc	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly	
245 250 255	
att tat gct gga gaa aat aga tca atg atg gtt agc aat tgc ttg ttt	816
Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gcg att ttg ctc tct aac aag tcg gga gac cgg	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac aag cta gtt cac acg gtc cga acg cat act gga	912
Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	
gct gat gac aag tct ttt cga tgt gtg caa caa gaa gac gat gag agc	960
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser	
305 310 315 320	
ggc aaa atc gga gtt tgt ctg tca aag gac ata acc aat gtt gcg ggg	1008
Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly	
325 330 335	
aca aca ctt acg aaa aat ata gca aca ttg ggt ccg ttg att ctt cct	1056
Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
tta agc gaa aag ttt ctt ttt ttc gct acc ttc gtc gcc aag aaa ctt	1104
Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu	
355 360 365	
cta aag gat aaa atc aag cat tac tat gtt ccg gat ttc aag ctt gct	1152
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala	
370 375 380	
gtt gac cat ttc tgt att cat gcc gga ggc aga gcc gtg atc gat gag	1200
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu	
385 390 395 400	
cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga	1248
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg	
405 410 415	
tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
420 425 430	
gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa	1344
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
435 440 445	
gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt	1392
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val	

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450          455          460
tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa      1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
465          470          475          480

cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag      1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
485          490          495

tca aag act cat gtc caa aac ggt cgg tcc taatttgatg tatctgagtg      1538
Ser Lys Thr His Val Gln Asn Gly Arg Ser
500          505

ccaacggttta ctttgtcttt cctttctttt attgggttatg aattagatgt ttactaatgt      1598
tcctctctttt ttcggtataa ataaagaagt tcaattcttc ctatagtttc aaacgcgatt      1658
ttaagcggtt ctatttaggt ttacatgaat ttctttttaca aaccatcttt t      1709

<210> 36
<211> 506
<212> PRT
<213> Artificial Sequence

<220>
<223> 506 amino acids from A. thaliana FAE1 (SEQ ID
      NO:2) having a mutation at residue 92; designated
      At K92R; hypothetical

<400> 36
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1          5          10          15
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
20          25          30
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
35          40          45
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe
50          55          60
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val
65          70          75          80
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Arg Val Ser Val Ser
85          90          95
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser
100         105         110
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys
115         120         125
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly
130         135         140
Leu Ile His Val Pro Pro Arg Lys Thr Phe Ala Ala Ser Arg Glu Glu
145         150         155         160
Thr Glu Lys Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Glu Asn Thr
165         170         175
Lys Val Asn Pro Arg Glu Ile Gly Ile Leu Val Val Asn Ser Ser Met
180         185         190
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys
195         200         205
Leu Arg Ser Asn Ile Lys Ser Phe Asn Leu Gly Gly Met Gly Cys Ser
210         215         220

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Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His
225                230                235                240
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Gln Gly
                245                250                255
Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe
                260                265                270
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Ser Gly Asp Arg
                275                280                285
Arg Arg Ser Lys Tyr Lys Leu Val His Thr Val Arg Thr His Thr Gly
                290                295                300
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Glu Asp Asp Glu Ser
305                310                315                320
Gly Lys Ile Gly Val Cys Leu Ser Lys Asp Ile Thr Asn Val Ala Gly
                325                330                335
Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
                340                345                350
Leu Ser Glu Lys Phe Leu Phe Phe Ala Thr Phe Val Ala Lys Lys Leu
                355                360                365
Leu Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
370                375                380
Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
385                390                395                400
Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
                405                410                415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
                420                425                430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
                435                440                445
Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
450                455                460
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
465                470                475                480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
                485                490                495
Ser Lys Thr His Val Gln Asn Gly Arg Ser
                500                505

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<210> 37

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 762 bp from A. thaliana FAE1 (SEQ ID NO:1) and
3' 759 bp from B. napus elongase KCS (SEQ ID NO:3)
and having a mutation at position 920; designated
At254 G307D; hypothetical

<221> CDS

<222> (1)...(1518)

<400> 37

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atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
1             5             10             15

```

48

```

ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa

```

96

Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	
		20						25					30			
gcc	tct	cgg	ctt	acc	ata	aac	gat	ctc	cac	aac	ttc	ctt	tcc	tat	ctc	144
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	
		35					40					45				
caa	cac	aac	ctt	ata	aca	gta	act	tta	ctc	ttt	gct	ttc	act	gtt	ttc	192
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	
	50					55					60					
ggt	ttg	gtt	ctc	tac	atc	gta	acc	cga	ccc	aat	ccg	gtt	tat	ctc	gtt	240
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	
65					70					75					80	
gac	tac	tcg	tgt	tac	ctt	cca	cca	ccg	cat	ctc	aaa	gtt	agt	gtc	tct	288
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser	
			85						90					95		
aaa	gtc	atg	gat	att	ttc	tac	caa	ata	aga	aaa	gct	gat	act	tct	tca	336
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	
			100					105					110			
cgg	aac	gtg	gca	tgt	gat	gat	ccg	tcc	tcg	ctc	gat	ttc	ctg	agg	aag	384
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys	
		115					120					125				
att	caa	gag	cgt	tca	ggt	cta	ggt	gat	gag	acg	tac	agt	cct	gag	gga	432
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly	
	130					135					140					
ctc	att	cac	gta	cca	ccg	cgg	aag	act	ttt	gca	gcg	tca	cgt	gaa	gag	480
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu	
145					150					155					160	
aca	gag	aag	gtt	atc	atc	ggt	gcg	ctc	gaa	aat	cta	ttc	gag	aac	acc	528
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Glu	Asn	Thr	
				165				170						175		
aaa	gtt	aac	cct	aga	gag	att	ggt	ata	ctt	gtg	gtg	aac	tca	agc	atg	576
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	
			180					185					190			
ttt	aat	cca	act	cct	tcg	cta	tcc	gct	atg	gtc	gtt	aat	act	ttc	aag	624
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	
		195					200					205				
ctc	cga	agc	aac	atc	aaa	agc	ttt	aat	cta	gga	gga	atg	ggt	tgt	agt	672
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	
	210					215					220					
gct	ggt	gtt	att	gcc	att	gat	ttg	gct	aaa	gac	ttg	ttg	cat	gtt	cat	720
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	
225					230					235					240	
aaa	aac	act	tat	gct	ctc	gtg	gtg	agc	aca	gag	aac	atc	act	tat	aac	768
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	

			245				250				255							
att	tac	gct	ggt	gat	aat	agg	tcc	atg	atg	gtt	tca	aat	tgc	ttg	ttc	816		
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe			
			260				265				270							
cgt	gtt	ggt	ggg	gcc	gct	att	ttg	ctc	tcc	aac	aag	cct	gga	gat	cgt	864		
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg			
			275				280				285							
aga	cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	gtt	cga	acg	cat	acc	gga	912		
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly			
			290				295				300							
gct	gac	gac	aag	tct	ttt	cgt	tgc	gtg	caa	caa	gga	gac	gat	gag	aac	960		
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn			
305			310				315				320							
ggc	aaa	atc	gga	gtg	agt	ttg	tcc	aag	gac	ata	acc	gat	gtt	gct	ggt	1008		
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly			
			325				330				335							
cga	acg	gtt	aag	aaa	aac	ata	gca	acg	ttg	ggt	ccg	ttg	att	ctt	ccg	1056		
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro			
			340				345				350							
tta	agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	ttc	atg	ggc	aag	aaa	ctt	1104		
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu			
			355				360				365							
ttc	aaa	gat	aaa	atc	aaa	cat	tac	tac	gtc	ccg	gat	ttc	aaa	ctt	gct	1152		
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala			
			370				375				380							
att	gac	cat	ttt	tgt	ata	cat	gcc	gga	ggc	aga	gcc	gtg	att	gat	gtg	1200		
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val			
385			390				395				400							
cta	gag	aag	aac	cta	gcc	cta	gca	ccg	atc	gat	gta	gag	gca	tca	aga	1248		
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg			
			405				410				415							
tca	acg	tta	cat	aga	ttt	gga	aac	act	tca	tct	agc	tca	ata	tgg	tat	1296		
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr			
			420				425				430							
gag	ttg	gca	tac	ata	gaa	gca	aaa	gga	agg	atg	aag	aaa	ggt	aat	aaa	1344		
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys			
			435				440				445							
gtt	tgg	cag	att	gct	tta	ggg	tca	ggc	ttt	aag	tgt	aac	agt	gca	gtt	1392		
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val			
			450				455				460							
tgg	gtg	gct	cta	aac	aat	gtc	aaa	gct	tcg	aca	aat	agt	cct	tgg	gaa	1440		
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu			
465			470				475				480							


```
tca gag act cgt gtc caa aac ggt cgg tcc taa      1521
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
          500                      505
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<210> 38
<211> 506
<212> PRT
<213> Artificial Sequence
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<220>
<223> 5' 254 amino acids from A. thaliana FAE1 (SEQ ID
      NO:2) and 3' 252 amino acids from B. napus
      elongase KCS (SEQ ID NO:4) having a mutation at
      residue 307; designated At254 G307D; hypothetical
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<400> 38																	
Met 1	Thr	Ser	Val	Asn 5	Val	Lys	Leu	Leu	Tyr 10	Arg	Tyr	Val	Leu	Thr 15	Asn		
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys		
			20			25			30								
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu		
			35			40			45								
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe		
50			55			60			65								
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val		
65				70			75			80							
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser		
			85			90			95								
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser		
			100			105			110								
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys		
115			120			125			130								
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly		
135			140			145			150								
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu		
145	155			160			165			170							
Thr	Glu	Lys	Val	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Glu	Asn	Thr			
			175			180			185			190					
Lys	Val	Asn	Pro	Arg	Glu	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met		
195			200			205			210			215					
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys		
			220			225			230			235					
Leu	Arg	Ser	Asn	Ile	Lys	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser		
240			245			250			255			260					
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His		
225	230			235			240			245			250				
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn		
			255			260			265			270					
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe		
265			270			275			280			285					
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg		

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      275              280              285
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly
 290              295              300
Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
305              310              315              320
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
      325              330              335
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
      340              345              350
Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
      355              360              365
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
      370              375              380
Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
385              390              395              400
Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
      405              410              415
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
      420              425              430
Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
      435              440              445
Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
      450              455              460
Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
465              470              475              480
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
      485              490              495
Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
      500              505

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<210> 39

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 519 bp from A. thaliana FAE1 (SEQ ID NO:1) and
3' 1002 bp from B. napus elongase KCS (SEQ ID
NO:3) and having a mutation at position 920;
designated At173 G307D

<221> CDS

<222> (1)...(1518)

<400> 39

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atg acg tcc gtt aac gtt aag ctc ctt tac cgt tac gtc tta acc aac      48
Met Thr Ser Val Asn Val Lys Leu Leu Tyr Arg Tyr Val Leu Thr Asn
 1              5              10              15

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ttt ttc aac ctc tgt ttg ttc ccg tta acg gcg ttc ctc gcc gga aaa      96
Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys
 20              25              30

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gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc      144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu
 35              40              45

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caa	cac	aac	ctt	ata	aca	gta	act	tta	ctc	ttt	gct	ttc	act	gtt	ttc	192
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	
50						55				60						
ggt	ttg	gtt	ctc	tac	atc	gta	acc	cga	ccc	aat	ccg	gtt	tat	ctc	gtt	240
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	
65				70						75				80		
gac	tac	tcg	tgt	tac	ctt	cca	cca	ccg	cat	ctc	aaa	gtt	agt	gtc	tct	288
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser	
				85				90						95		
aaa	gtc	atg	gat	att	ttc	tac	caa	ata	aga	aaa	gct	gat	act	tct	tca	336
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	
		100				105						110				
cgg	aac	gtg	gca	tgt	gat	gat	ccg	tcc	tcg	ctc	gat	ttc	ctg	agg	aag	384
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys	
		115				120						125				
att	caa	gag	cgt	tca	ggg	cta	ggg	gat	gag	acg	tac	agt	cct	gag	gga	432
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly	
130						135				140						
ctc	att	cac	gta	cca	ccg	cgg	aag	act	ttt	gca	gcg	tca	cgt	gaa	gag	480
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu	
145				150						155				160		
aca	gag	aag	gtt	atc	atc	ggg	gcg	ctc	gaa	aat	cta	ttc	aag	aac	acc	528
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	
				165				170						175		
aac	gtt	aac	cct	aaa	gat	ata	ggg	ata	ctt	gtg	gtg	aac	tca	agc	atg	576
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	
		180				185						190				
ttt	aat	cca	act	cca	tcg	ctc	tcc	gcg	atg	gtc	gtt	aac	act	ttc	aag	624
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	
		195				200						205				
ctc	cga	agc	aac	gta	aga	agc	ttt	aac	ctt	ggg	ggc	atg	ggg	tgt	agt	672
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	
210						215				220						
gcc	ggc	gtt	ata	gcc	att	gat	cta	gca	aag	gac	ttg	ttg	cat	gtc	cat	720
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	
225				230						235				240		
aaa	aat	acg	tat	gct	ctt	gtg	gtg	agc	aca	gag	aac	atc	act	tat	aac	768
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	
				245				250						255		
att	tac	gct	ggg	gat	aat	agg	tcc	atg	atg	gtt	tca	aat	tgc	ttg	ttc	816
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	
		260														

Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	
		275					280					285				
aga	cgg	tcc	aag	tac	gag	cta	gtt	cac	acg	gtt	cga	acg	cat	acc	gga	912
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	
		290				295					300					
gct	gac	gac	aag	tct	ttt	cgt	tg	gtg	caa	caa	gga	gac	gat	gag	aac	960
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	
305					310					315					320	
ggc	aaa	atc	gga	gtg	agt	ttg	tcc	aag	gac	ata	acc	gat	gtt	gct	ggt	1008
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	
				325					330					335		
cga	acg	gtt	aag	aaa	aac	ata	gca	acg	ttg	ggg	ccg	ttg	att	ctt	ccg	1056
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro	
			340					345					350			
tta	agc	gag	aaa	ctt	ctt	ttt	ttc	gtt	acc	ttc	atg	ggc	aag	aaa	ctt	1104
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu	
			355				360					365				
ttc	aaa	gat	aaa	atc	aaa	cat	tac	tac	gtc	ccg	gat	ttc	aaa	ctt	gct	1152
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	
		370				375					380					
att	gac	cat	ttt	tgt	ata	cat	gcc	gga	ggc	aga	gcc	gtg	att	gat	gtg	1200
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Val	
385					390					395					400	
cta	gag	aag	aac	cta	gcc	cta	gca	ccg	atc	gat	gta	gag	gca	tca	aga	1248
Leu	Glu	Lys	Asn	Leu	Ala	Leu	Ala	Pro	Ile	Asp	Val	Glu	Ala	Ser	Arg	
				405					410					415		
tca	acg	tta	cat	aga	ttt	gga	aac	act	tca	tct	agc	tca	ata	tgg	tat	1296
Ser	Thr	Leu	His	Arg	Phe	Gly	Asn	Thr	Ser	Ser	Ser	Ser	Ile	Trp	Tyr	
			420					425						430		
gag	ttg	gca	tac	ata	gaa	gca	aaa	gga	agg	atg	aag	aaa	ggg	aat	aaa	1344
Glu	Leu	Ala	Tyr	Ile	Glu	Ala	Lys	Gly	Arg	Met	Lys	Lys	Gly	Asn	Lys	
		435					440						445			
gtt	tgg	cag	att	gct	tta	ggg	tca	ggc	ttt	aag	tgt	aac	agt	gca	gtt	1392
Val	Trp	Gln	Ile	Ala	Leu	Gly	Ser	Gly	Phe	Lys	Cys	Asn	Ser	Ala	Val	
		450				455					460					
tgg	gtg	gct	cta	aac	aat	gtc	aaa	gct	tcg	aca	aat	agt	cct	tgg	gaa	1440
Trp	Val	Ala	Leu	Asn	Asn	Val	Lys	Ala	Ser	Thr	Asn	Ser	Pro	Trp	Glu	
465					470					475					480	
cac	tg	atc	gac	aga	tac	ccg	gtc	aaa	att	gat	tct	gat	tca	ggg	aag	1488
His	Cys	Ile	Asp	Arg	Tyr	Pro	Val	Lys	Ile	Asp	Ser	Asp	Ser	Gly	Lys	
				485				490						495		
tca	gag	act	cgt	gtc	caa	aac	ggg	cgg	tcc	taa						1521
Ser	Glu	Thr	Arg	Val	Gln	Asn	Gly	Arg	Ser							

500

505

<210> 40

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 173 amino acids from *A. thaliana* FAE1 (SEQ ID NO:2) and 3' 333 amino acids from *B. napus* elongase KCS (SEQ ID NO:4) having a mutation at residue 307; designated At173 G307D; hypothetical

<400> 40

Met	Thr	Ser	Val	Asn	Val	Lys	Leu	Leu	Tyr	Arg	Tyr	Val	Leu	Thr	Asn	1	5	10	15
Phe	Phe	Asn	Leu	Cys	Leu	Phe	Pro	Leu	Thr	Ala	Phe	Leu	Ala	Gly	Lys	20	25	30	
Ala	Ser	Arg	Leu	Thr	Ile	Asn	Asp	Leu	His	Asn	Phe	Leu	Ser	Tyr	Leu	35	40	45	
Gln	His	Asn	Leu	Ile	Thr	Val	Thr	Leu	Leu	Phe	Ala	Phe	Thr	Val	Phe	50	55	60	
Gly	Leu	Val	Leu	Tyr	Ile	Val	Thr	Arg	Pro	Asn	Pro	Val	Tyr	Leu	Val	65	70	75	80
Asp	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Pro	His	Leu	Lys	Val	Ser	Val	Ser	85	90	95	
Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Ile	Arg	Lys	Ala	Asp	Thr	Ser	Ser	100	105	110	
Arg	Asn	Val	Ala	Cys	Asp	Asp	Pro	Ser	Ser	Leu	Asp	Phe	Leu	Arg	Lys	115	120	125	
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	Tyr	Ser	Pro	Glu	Gly	130	135	140	
Leu	Ile	His	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ser	Arg	Glu	Glu	145	150	155	160
Thr	Glu	Lys	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr	165	170	175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met	180	185	190	
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys	195	200	205	
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser	210	215	220	
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His	225	230	235	240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn	245	250	255	
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	260	265	270	
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg	275	280	285	
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly	290	295	300	
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn	305	310	315	320
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly	325	330	335	

Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Val
 385 390 395 400
 Leu Glu Lys Asn Leu Ala Leu Ala Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Val Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Asn Asn Val Lys Ala Ser Thr Asn Ser Pro Trp Glu
 465 470 475 480
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Ser Gly Lys
 485 490 495
 Ser Glu Thr Arg Val Gln Asn Gly Arg Ser
 500 505

<210> 41

<211> 1521

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' 1197 bp from B. napus elongase KCS (SEQ ID
 NO:3) and 3' 324 bp from A. thaliana FAE1 (SEQ ID
 NO:1) and having a mutation at nucleotide position
 920; designated Bn399 G307D; hypothetical

<221> CDS

<222> (1)...(1518)

<400> 41

atg acg tcc att aac gtt aag ctc ctt tac cat tac gtc ata acc aac 48
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 1 5 10 15

ctt ttc aac ctt tgc ttc ttt ccg tta acg gcg atc gtc gcc gga aaa 96
 Leu Phe Asn Leu Cys Phe Phe Pro Leu Thr Ala Ile Val Ala Gly Lys
 20 25 30

gcc tat cgg ctt acc ata gac gat ctt cac cac tta tac tat tcc tat 144
 Ala Tyr Arg Leu Thr Ile Asp Asp Leu His His Leu Tyr Tyr Ser Tyr
 35 40 45

ctc caa cac aac ctc ata acc atc gct cca ctc ttt gcc ttc acc gtt 192
 Leu Gln His Asn Leu Ile Thr Ile Ala Pro Leu Phe Ala Phe Thr Val
 50 55 60

ttc ggt tcg gtt ctc tac atc gca acc ccg ccc aaa ccg gtt tac ctc 240
 Phe Gly Ser Val Leu Tyr Ile Ala Thr Arg Pro Lys Pro Val Tyr Leu
 65 70 75 80

gtt gag tac tca tgc tac ctt cca cca acg cat tgt aga tca agt atc	288
Val Glu Tyr Ser Cys Tyr Leu Pro Pro Thr His Cys Arg Ser Ser Ile	
85 90 95	
tcc aag gtc atg gat atc ttt tat caa gta aga aaa gct gat cct tct	336
Ser Lys Val Met Asp Ile Phe Tyr Gln Val Arg Lys Ala Asp Pro Ser	
100 105 110	
cgg aac ggc acg tgc gat gac tcg tcg tgg ctt gac ttc ttg agg aag	384
Arg Asn Gly Thr Cys Asp Asp Ser Ser Trp Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gaa cgt tca ggt cta ggc gat gaa act cac ggg ccc gag ggg	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr His Gly Pro Glu Gly	
130 135 140	
ctg ctt cag gtc cct ccc cgg aag act ttt gcg gcg gcg cgt gaa gag	480
Leu Leu Gln Val Pro Pro Arg Lys Thr Phe Ala Ala Ala Arg Glu Glu	
145 150 155 160	
acg gag caa gtt atc att ggt gcg cta gaa aat cta ttc aag aac acc	528
Thr Glu Gln Val Ile Ile Gly Ala Leu Glu Asn Leu Phe Lys Asn Thr	
165 170 175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg	576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met	
180 185 190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag	624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys	
195 200 205	
ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt	672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser	
210 215 220	
gcc ggc gtt ata gcc att gat cta gca aag gac ttg ttg cat gtc cat	720
Ala Gly Val Ile Ala Ile Asp Leu Ala Lys Asp Leu Leu His Val His	
225 230 235 240	
aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac	768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn	
245 250 255	
att tac gct ggt gat aat agg tcc atg atg gtt tca aat tgc ttg ttc	816
Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
cgt gtt ggt ggg gcc gct att ttg ctc tcc aac aag cct gga gat cgt	864
Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg	
275 280 285	
aga cgg tcc aag tac gag cta gtt cac acg gtt cga acg cat acc gga	912
Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly	
290 295 300	

gct gac gac aag tct ttt cgt tgc gtg caa caa gga gac gat gag aac 960
 Ala Asp Asp Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn
 305 310 315 320

 ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt 1008
 Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly
 325 330 335

 cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg 1056
 Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro
 340 345 350

 tta agc gag aaa ctt ctt ttt ttc gtt acc ttc atg ggc aag aaa ctt 1104
 Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu
 355 360 365

 ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct 1152
 Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala
 370 375 380

 att gac cat ttt tgt ata cat gcc gga ggc aga gcc gtg atc gat gag 1200
 Ile Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu
 385 390 395 400

 cta gag aag aac tta gga cta tcg ccg atc gat gtg gag gca tct aga 1248
 Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415

 tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat 1296
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430

 gaa tta gca tac ata gag gca aag gga aga atg aag aaa ggg aat aaa 1344
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445

 gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt 1392
 Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460

 tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa 1440
 Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
 465 470 475 480

 cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag 1488
 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
 485 490 495

 tca aag act cat gtc caa aac ggt cgg tcc taa 1521
 Ser Lys Thr His Val Gln Asn Gly Arg Ser
 500 505

<210> 42

<211> 506

<212> PRT

<213> Artificial Sequence

<220>

<223> 5' 399 amino acids from B. napus elongase KCS (SEQ
ID NO:3) and 3' 107 amino acids from A. thaliana
FAE1 (SEQ ID NO:1) having a mutation at residue
306; designated Bn399 G307D; hypothetical

<400> 42

Met	Thr	Ser	Ile	Asn	Val	Lys	Leu	Leu	Tyr	His	Tyr	Val	Ile	Thr	Asn
1				5					10					15	
Leu	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	Thr	Ala	Ile	Val	Ala	Gly	Lys
			20					25					30		
Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	Ser	Tyr
		35				40						45			
Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	Thr	Val
	50					55					60				
Phe	Gly	Ser	Val	Leu	Tyr	Ile	Ala	Thr	Arg	Pro	Lys	Pro	Val	Tyr	Leu
65					70				75						80
Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile
			85						90					95	
Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser
			100					105					110		
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys
		115					120					125			
Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly
	130					135					140				
Leu	Leu	Gln	Val	Pro	Pro	Arg	Lys	Thr	Phe	Ala	Ala	Ala	Arg	Glu	Glu
145					150					155					160
Thr	Glu	Gln	Val	Ile	Ile	Gly	Ala	Leu	Glu	Asn	Leu	Phe	Lys	Asn	Thr
				165				170						175	
Asn	Val	Asn	Pro	Lys	Asp	Ile	Gly	Ile	Leu	Val	Val	Asn	Ser	Ser	Met
			180				185						190		
Phe	Asn	Pro	Thr	Pro	Ser	Leu	Ser	Ala	Met	Val	Val	Asn	Thr	Phe	Lys
		195				200						205			
Leu	Arg	Ser	Asn	Val	Arg	Ser	Phe	Asn	Leu	Gly	Gly	Met	Gly	Cys	Ser
	210					215					220				
Ala	Gly	Val	Ile	Ala	Ile	Asp	Leu	Ala	Lys	Asp	Leu	Leu	His	Val	His
225					230				235						240
Lys	Asn	Thr	Tyr	Ala	Leu	Val	Val	Ser	Thr	Glu	Asn	Ile	Thr	Tyr	Asn
				245					250				255		
Ile	Tyr	Ala	Gly	Asp	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe
			260					265					270		
Arg	Val	Gly	Gly	Ala	Ala	Ile	Leu	Leu	Ser	Asn	Lys	Pro	Gly	Asp	Arg
		275					280						285		
Arg	Arg	Ser	Lys	Tyr	Glu	Leu	Val	His	Thr	Val	Arg	Thr	His	Thr	Gly
		290				295					300				
Ala	Asp	Asp	Lys	Ser	Phe	Arg	Cys	Val	Gln	Gln	Gly	Asp	Asp	Glu	Asn
305					310					315					320
Gly	Lys	Ile	Gly	Val	Ser	Leu	Ser	Lys	Asp	Ile	Thr	Asp	Val	Ala	Gly
			325						330					335	
Arg	Thr	Val	Lys	Lys	Asn	Ile	Ala	Thr	Leu	Gly	Pro	Leu	Ile	Leu	Pro
			340					345					350		
Leu	Ser	Glu	Lys	Leu	Leu	Phe	Phe	Val	Thr	Phe	Met	Gly	Lys	Lys	Leu
		355				360						365			
Phe	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala
	370					375					380				
Ile	Asp	His	Phe	Cys	Ile	His	Ala	Gly	Gly	Arg	Ala	Val	Ile	Asp	Glu

385 390 395 400
 Leu Glu Lys Asn Leu Gly Leu Ser Pro Ile Asp Val Glu Ala Ser Arg
 405 410 415
 Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr
 420 425 430
 Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys
 435 440 445
 Ala Trp Gln Ile Ala Leu Gly Ser Gly Phe Lys Cys Asn Ser Ala Val
 450 455 460
 Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln
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 His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys
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 Ser Lys Thr His Val Gln Asn Gly Arg Ser
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25

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